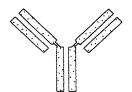
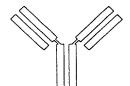
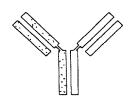
Monospecific Bivalent

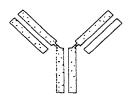
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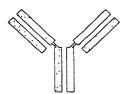


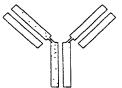


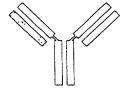


Monospecific Monovalent

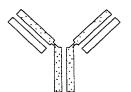


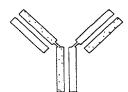






"Inactive"





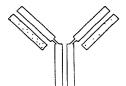


FIG. I

BsF(ab')₂ CHEMICALLY COUPLED RODENT FRAGMENTS

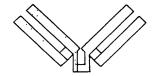


FIG. 2A

BsF(ab¹)₂
CHEMICALLY COUPLED
E. coli DERIVED FRAGMENTS

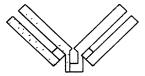


FIG.2B

BsF(ab')₂ LEUCINE ZIPPER ASSEMBLED

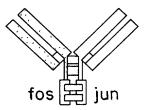
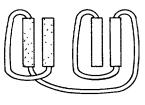
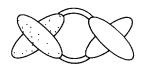


FIG. 2C



sFv DIMER

FIG. 2E



DIABODY

FIG. 2D

RECEPTOR



FIG.3A

IgG1-HEAVY CHAIN

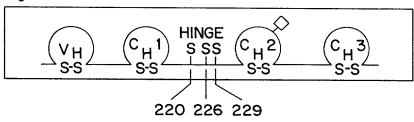


FIG.3B

IMMUNOADHESIN

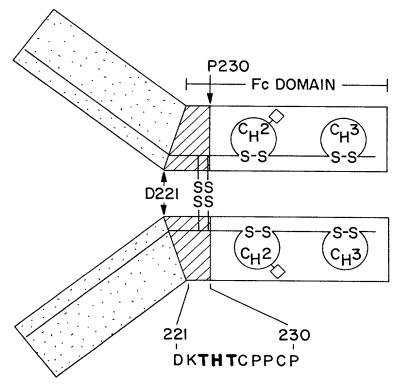
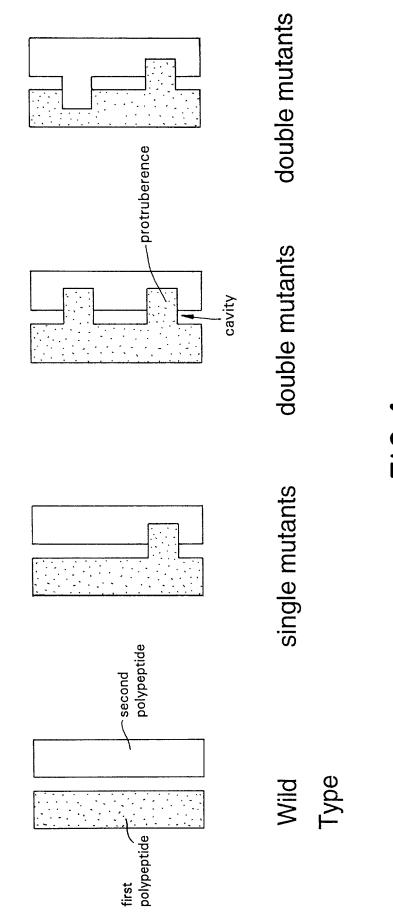


FIG. 3C



F16.4

edge, interface

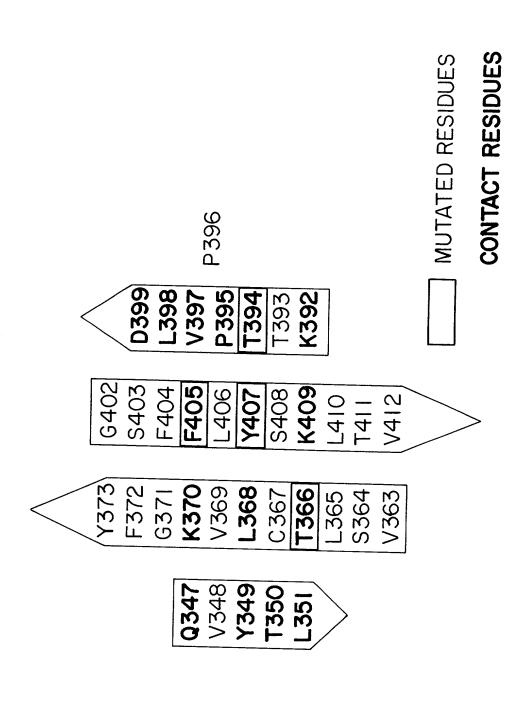
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BiBIBI
                       ві
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IqG
IgA
    GNTFRPQVHLLPPPSEELALBZL
IgD
    QAPVKLSLNLLASSDP--PEAA
IqE
    G P R A A P E V Y A F A T P E W P G S R D K
IgM
    - D Z B T A I R V F A I P P S F ASIFL T K S
                  350
                                 360
    middle, interface
                           exterior
    BIBIBIBi
                          В
                             В
                                 В
    V S L T C L V K G F Y P S D I A V E W E S N
IgG
IqA
      T L T C L A R G F S P K D V L V R W L Q G
    SWLLCEVSGFSPPNILLMWL EDO
IqD
IgE
    RTLACLIQNFMPEDISVQWLHN
IqM
    TKLTCLVTDLTTYBSVTISWTRZ
               370
                              380
                  edge, interface
                      Ι
                          i
                               I
    D - G Q P E N N Y K T T P P V/M L D S D G S
IgG
IgA
    SQELPREKYLTWASR
                             O Z PSOGTTT
IqD
    REVNTSGFAPARPP
                             QPGSTT
    EVQLPDARHSTTQPR
IgE
                             KTKGSG
IqM
       - G E A V K T H T B I S Z
                             SHPBAT
               390
                                400
     middle, interface
                                    exterior
               вів
    BIBIBI
                          В
                                    В
                                       В
                                          В
      FLYSK/RLTVDKSRWQQGNVFSCSVM
IgG
IgA
    F A V T S
            I
               LRVAAEDWKKGDTFSCMVG
IqD
    FWAWSV
               LRVPAPPSPOPATYT
                                      CVVS
    F F V F S R
               LEVTRAEWEQKDEFICRAV
IgE
               ASICEBBWBSGERFTCTVT
MpI
    F S A V G E
               410
                              420
                  exterior
    В
                 b
                    b
                       b
IqG
    H E A L H N H Y T Q K S L S L S P G K
IgA
    HEALPLAFTQKTIDRLAGK
IqD
    HED-SRTLLNASRSLEVSY
                                      FIG.5
    H E A ASP S Q T V Q R A V S V N P G K
IgE
    HTDLPSPLKQTISRPK---
IgM
     430
                     440
```

MIDDLE 4390 5 1 7 C 5 1 7 C 5 1 7 C	390 L H C L H C L H C L H C L H C	→ MMM →	
380 - M T K N Q (V S - M T K N Q V S - M T K N Q V S - M T K N Q V S	80 - M A K D K V S - M T K K Z F S - L S R K D V S - M S K K K V S	- G Z P Z B N Y Q P E N N Y Q P E N N Y Q P E N N Y	
PPSREE PPSREE PPSREE 	m 国のの*・(410 E W E S - B D E W E S - N G E W E S - S G E W Z S - N G	E W Q W - B G E W T S - N G E W T S - N G E W E R - N G
EDGE E P Q V Y T L E P Q V Y T L E P Q V Y T L E P Q V Y T L E P Q V Y T L	370 A P Q V Y T I A P Q V Y V L A P Q V Y T I T P Q V Y T I T P Q V Y T I	- Q S	E D I T V A E I A V G D I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V E A I S V -
361 G - OPR G - OPR G - OPR G - OPR	361 G - R P I G - P V F G - L V F G - R A C ************************************	LVKGFYPLVKGFYPLVKGFYPLVKGFYP	MITDFFP MITGFLP LVVGFNP LVTNFFS ***********
hIgG1 hIgG2 hIgG3 hIgG4	0611 0611 0611 0611 1661	hIgG1 hIgG2 hIgG3 hIgG4	mIgG1 mIgG2A mIgG2B mIgG3 ******

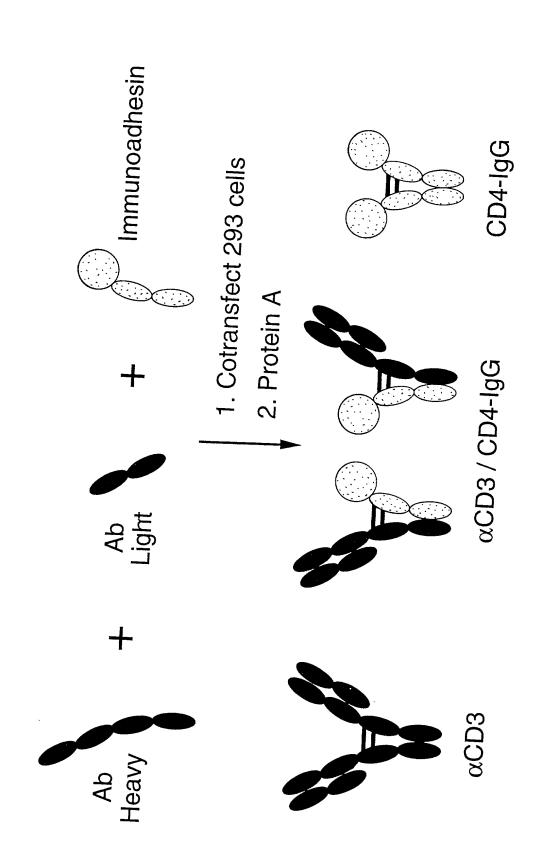
FIG.6A

MIDDLE $430 \qquad \downarrow \qquad \downarrow \qquad \downarrow \qquad \downarrow \qquad 450$ $S - D G S F F L Y S K L T V D K S R W Q Q$ $S - D G S F F L Y S K L T V D K S R W Q Q$ $S - D G S F F L Y S K L T V D K S R W Q Q$ $S - D G S F F L Y S R L T V D K S R W Q Q$	T - B G S Y F V Y S K L N V Q K S N W E A S - D G S Y F M Y S K L N W Z K S T W E R S - D G S Y F I Y S K L N M K T S K W E K S - D G T Y F L Y S K L T V D T D S W L Q S W L Q S W L Q W E K S + X * X * X * X * X * X * X * X * X * X	V L H E G L H N H H T E K S L S H S P G K V V H E G L H N H L T T K T F S R S L G K V R H E G L K N Y Y L K K T I S R S P G K V V H E A L H N H H T Q K N L S R S P G K ***********************************
EDGE TTPPVLDS- TTPPMLDS- TTPPMLDS- TTPPMLDS-	A N T Q P I M B T - B B T A T V L D S - D B T A P V L D S - D N T P P I L D S - D **********************************	G N T F T C S V L H E G S L F A C S V V H E B T D S F S C N V R H E G E I F T C S V V H E *******************************
higg higg higg	mIgG1 mIgG2 mIgG3 **** hIgG hIgE hIgG3 hIgG3	mIgG2 mIgG2; mIgG3; ****

F16.6B



F16.7



F16.8

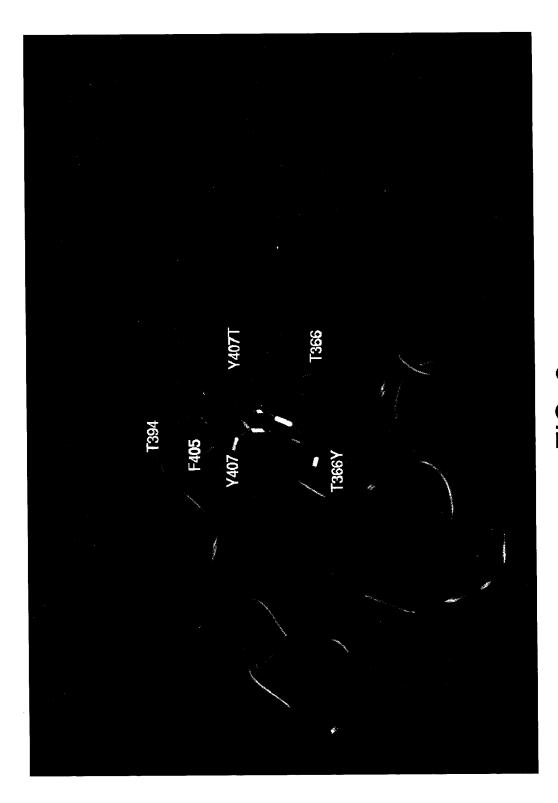


FIG. 9

